

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:47:41 ; Search time 30.9604 Seconds
(without alignments)
711.279 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLVLVLVLSWLPFGGALSIA.....DTGVSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	308	3	US-08-775-882-4 Sequence 4, Appli
2	1550	100.0	308	3	US-08-775-882-6 Sequence 6, Appli
3	1550	100.0	308	4	US-09-276-600-6 Sequence 6, Appli
4	1550	100.0	308	4	US-09-976-594-449 Sequence 449, App
5	1550	100.0	308	4	US-09-919-039-192 Sequence 192, Appli
6	1546	99.7	308	3	US-08-927-433-9 Sequence 9, Appli
7	1546	99.7	314	4	US-09-949-016-10118 Sequence 10118, A
8	1542	99.5	295	2	US-08-411-607A-2 Sequence 2, Appli
9	1542	99.5	295	4	US-09-361-741-2 Sequence 2, Appli
10	1542	99.5	295	4	US-09-461-418-2 Sequence 2, Appli
11	1531	98.8	308	4	US-09-949-016-6559 Sequence 6559, Ap
12	659	42.5	119	4	US-08-626-185-4 Sequence 4, Appli
13	624	40.3	112	3	US-08-927-433-8 Sequence 8, Appli
14	624	40.3	112	3	US-08-927-433-10 Sequence 10, Appli
15	545	35.2	99	3	US-08-775-882-2 Sequence 2, Appli
16	460	29.7	115	4	US-09-463-931-2 Sequence 2, Appli
17	229	14.8	513	2	US-08-459-346-19 Sequence 19, Appli
18	229	14.8	513	2	US-07-989-847-8 Sequence 8, Appli
19	229	14.8	513	3	US-08-889-419-19 Sequence 19, Appli
20	229	14.8	513	3	US-08-489-411-8 Sequence 8, Appli
21	229	14.8	513	3	US-08-402-542-19 Sequence 19, Appli
22	229	14.8	513	4	US-09-780-601A-8 Sequence 8, Appli
23	229	14.8	513	4	US-09-949-016-6118 Sequence 6118, Ap
24	229	14.8	513	5	PCT-US93-07189-19 Sequence 19, Appli
25	229	14.8	513	6	5187076-6 Patent No. 5187076
26	229	14.8	513	6	5187076-6 Patent No. 5187076
27	229	14.8	563	4	US-09-949-016-11259 Sequence 11259, A

28	221	14.3	372	1	US-08-278-729A-33	Sequence 33, Appli
29	221	14.3	372	1	US-08-155-343A-33	Sequence 33, Appli
30	221	14.3	372	1	US-08-406-672-33	Sequence 33, Appli
31	221	14.3	372	1	US-08-643-563A-33	Sequence 33, Appli
32	221	14.3	372	1	US-08-643-763A-33	Sequence 33, Appli
33	221	14.3	372	1	US-08-462-623-33	Sequence 33, Appli
34	221	14.3	372	1	US-08-451-953A-33	Sequence 33, Appli
35	221	14.3	372	2	US-08-459-346-15	Sequence 15, Appli
36	221	14.3	372	2	US-08-445-468A-33	Sequence 33, Appli
37	221	14.3	372	2	US-08-461-397A-33	Sequence 33, Appli
38	221	14.3	372	2	US-08-912-088-33	Sequence 33, Appli
39	221	14.3	372	3	US-08-278-730A-33	Sequence 33, Appli
40	221	14.3	372	3	US-08-889-419-15	Sequence 15, Appli
41	221	14.3	372	3	US-08-445-467-33	Sequence 33, Appli
42	221	14.3	372	3	US-08-480-515A-33	Sequence 33, Appli
43	221	14.3	372	3	US-09-170-936-33	Sequence 33, Appli
44	221	14.3	372	3	US-08-402-542-15	Sequence 15, Appli
45	221	14.3	372	3	US-08-461-113-33	Sequence 33, Appli

ALIGNMENTS

RESULT 1

US-08-775-882-4

/ Sequence 4, Application US/08775882

/ Patent No. 6180602

/ GENERAL INFORMATION:

/ APPLICANT: KATO, Seishi

/ APPLICANT: OH, Suwan

/ APPLICANT: SEKINE, Shingo

/ APPLICANT: SAEKI, Mihoro

/ APPLICANT: KOBAYASHI, Midori

/ APPLICANT: YADA, Mika

/ APPLICANT: TSUJI, Tomoko

/ APPLICANT: OHMORI, Hitoshi

/ TITLE OF INVENTION: HUMAN NOVEL CDNA, TGF-BETA SUPERFAMILY

/ TITLE OF INVENTION: PROTEIN ENCODED THEREBY AND THE USE AS IMMUNOSUPPRESSIVE

/ NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Foley & Lardner

/ STREET: 3000 K Street, N.W., Suite 500

/ CITY: Washington

/ STATE: D.C.

/ COUNTRY: USA

/ ZIP: 20007-5109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/775,882

/ FILING DATE: 02-JAN-1997

/ CLASSIFICATION: 514

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/390,207

/ FILING DATE: 16-FEB-1995

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/379,441

/ FILING DATE: 03-FEB-1995

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 5-61431

/ FILING DATE: 26-FEB-1993

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 4-327619

/ FILING DATE: 13-NOV-1992

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 4-208077

/ FILING DATE: 04-AUG-1992

/ ATTORNEY/AGENT INFORMATION:

/ NAME: WEGNER, Harold C.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:49:12 ; Search time 85.2871 Seconds
(without alignments)
1245.908 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLLVLLVLSWLPHGALSLA.....DTGVSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
3: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
4: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
5: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
6: /cgm2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
7: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
8: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
9: /cgm2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pap.*
10: /cgm2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pap.*
11: /cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
12: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
13: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
14: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
15: /cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
16: /cgm2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pap.*
17: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
18: /cgm2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pap.*
19: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
20: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
21: /cgm2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	308	9	US-09-276-600-6
2	1550	100.0	308	9	US-09-981-353-188
3	1550	100.0	308	10	US-09-919-039-192
4	1550	100.0	308	13	US-10-000-628-6
5	1550	100.0	308	15	US-10-257-597-2
6	1546	99.7	308	16	US-10-425-115-229584
7	1542	99.5	295	9	US-09-361-741-2
8	1538	99.5	308	15	US-10-211-689-72
9	1538	99.2	295	14	US-10-270-377-2
10	1537	99.2	308	15	US-10-257-597-1
11	1531	98.8	308	14	US-10-205-823-327
12	1531	98.8	308	14	US-10-021-660-113

13	1531	98.8	308	15	US-10-235-027-618	Sequence 618, Appl
14	1531	98.8	308	15	US-10-295-027-1379	Sequence 1379, Ap
15	1531	98.8	308	15	US-10-211-462-191	Sequence 191, Appl
16	1531	98.8	308	15	US-10-448-664-2	Sequence 2, Appl
17	1464	94.5	283	16	US-10-211-689-76	Sequence 76, Appl
18	884.5	57.1	298	9	US-09-789-919-68	Sequence 68, Appl
19	659	42.5	119	15	US-10-373-581-4	Sequence 4, Appl
20	540	34.8	102	15	US-10-211-689-74	Sequence 74, Appl
21	460	22.7	115	14	US-10-194-382-2	Sequence 2, Appl
22	244	15.7	45	16	US-10-408-765A-976	Sequence 976, Appl
23	229	14.8	513	14	US-10-122-026-19	Sequence 19, Appl
24	229	14.8	513	14	US-10-164-279-33	Sequence 33, Appl
25	229	14.8	513	15	US-10-366-345-38	Sequence 38, Appl
26	229	14.8	513	15	US-10-291-265-816	Sequence 816, Appl
27	229	14.8	513	15	US-10-375-150-8	Sequence 8, Appl
28	221	14.3	372	8	US-08-260-675-33	Sequence 33, Appl
29	221	14.3	372	10	US-09-952-318A-33	Sequence 33, Appl
30	221	14.3	372	14	US-10-122-026-15	Sequence 15, Appl
31	221	14.3	372	14	US-10-050-050-33	Sequence 33, Appl
32	221	14.3	372	14	US-10-164-279-49	Sequence 49, Appl
33	221	14.3	372	15	US-10-366-345-49	Sequence 49, Appl
34	221	14.3	372	15	US-10-295-027-244	Sequence 244, Appl
35	221	14.3	373	9	US-09-813-398-36	Sequence 36, Appl
36	221	14.3	373	16	US-10-826-324-36	Sequence 36, Appl
37	219.5	14.2	438	14	US-10-122-026-14	Sequence 14, Appl
38	218	14.1	437	9	US-09-784-911-4	Sequence 4, Appl
39	214.5	13.8	347	14	US-10-274-971-2	Sequence 2, Appl
40	212.5	13.7	281	15	US-10-375-150-12	Sequence 12, Appl
41	212.5	13.7	402	10	US-09-952-318A-21	Sequence 21, Appl
42	212.5	13.7	402	14	US-10-050-050-21	Sequence 21, Appl
43	212.5	13.7	402	14	US-10-164-279-45	Sequence 45, Appl
44	212.5	13.7	402	15	US-10-366-345-40	Sequence 40, Appl
45	212.5	13.7	403	9	US-09-813-398-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-276-600-6
; Sequence 6, Application: US/09276600
; Patent No. US20010010908A1
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Detecting Disease of the Prostate
; FILE REFERENCE: 6397 US 01
; CURRENT APPLICATION NUMBER: US/09/276,600
; CURRENT FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-276-600-6

Query Match 100.0%; Score 1550; DB 9; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLVLLVLSWLPHGALSLAASPPGSELHTDSRPFELKRYEDLLTRANQSW 60
Db 14 MLLVLLVLSWLPHGALSLAASPPGSELHTDSRPFELKRYEDLLTRANQSW 73
Qy 61 EDSDNDLVPAVAVRILTPFVRLGSGGHLHRIISRAALPEGLPEASRLHRLFRISPTASR 120

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:10 ; Search time 89.9604 Seconds
(without alignments)
1679.221 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLVLVLVSLWPHGGALSLA.....DTGVSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	308	1	GDFP_HUMAN
2	1546	99.7	308	2	Q9BWA0
3	911.5	58.8	303	1	GDFP_MOUSE
4	909.5	58.7	303	2	O6NX53
5	887.5	57.3	303	1	GDFP_RAT
6	255.5	16.5	387	2	Q869H8
7	240.5	15.5	373	2	Q98950
8	237.5	15.3	373	2	Q90723
9	230	14.8	350	2	Q645R0
10	229	14.8	513	1	BMP6_HUMAN
11	221	14.3	372	1	GDF1_HUMAN
12	220	14.2	506	2	Q811S4
13	218	14.1	461	1	GDF7_MOUSE
14	216	13.9	301	2	Q86RL7
15	216	13.9	435	1	BMP6_MOUSE
16	216	13.9	510	1	BMP6_MOUSE
17	215.5	13.9	365	2	O765I4
18	215	13.9	424	2	Q6P4J4
19	214.5	13.8	347	1	NODA_HUMAN
20	214.5	13.8	365	2	O02424
21	212.5	13.7	402	1	BMBB_HUMAN
22	212.5	13.7	402	2	O725V6
23	212	13.7	354	1	NODA_MOUSE
24	211.5	13.6	453	2	Q75RY1
25	210.5	13.6	453	1	GDF9_CAPHI
26	210	13.5	350	2	Q66KL4
27	210	13.5	354	2	Q8BH87
28	209.5	13.5	294	2	Q9BDW9
29	209.5	13.5	447	1	GDF7_CERAE
30	208.5	13.5	289	2	Q9XYQ8
31	208.5	13.5	450	1	QPD7_HUMAN

32	208	13.4	207	1	BMP6_RAT
33	208	13.4	417	2	Q9XIQ7
34	208	13.4	430	1	BMP7_MOUSE
35	207.5	13.4	453	1	GDF9_SHEEP
36	207	13.4	431	1	BMP7_HUMAN
37	207	13.4	441	2	Q6PUD1
38	207	13.4	441	2	Q7PZ17
39	207	13.4	452	2	Q6HA10
40	206.5	13.3	454	1	BMP5_HUMAN
41	205.5	13.3	361	2	O96504
42	205.5	13.3	424	2	Q9YGH7
43	205.5	13.3	446	2	Q7T288
44	205	13.2	452	1	BMP5_MOUSE
45	205	13.2	454	2	Q8CCB0

ALIGNMENTS

RESULT 1
ID_GDFF_HUMAN STANDARD; PRT; 308 AA.
AC Q99588; O14629; P78360; Q9NRT0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1).
DE Name=GDF15; Synonyms=MIC1, PDF, PLAB, PTGFB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroarcoma;
RX MEDLINE=98006316; PubMed=9348093;
RA Yokoyama-Kobayashi M., Saeki M., Sekine S., Kato S.;
RT "Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in placenta.";
RL J. Biochem. 122:622-626(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97470998; PubMed=9326641; DOI=10.1073/pnas.94.21.11514;
RA Bootcov M.R., Bauskin A.R., Valenzuela S.M., Moore A.G., Bansal M., He X.Y., Zhang H.P., Donnellan M., Mahler S., Pryor K., Walsh B.J., Nicholson R.C., Fairlie W.D., Por S.B., Robbins J.M., Breit S.N.;
RT "MIC-1, a novel macrophage inhibitory cytokine, is a divergent member of the TGF-beta superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11514-11519(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=98041637; PubMed=9375789; DOI=10.1016/S0167-4781(97)00122-X;
RA Hromas R., Hufford M., Sutton J., Xu D., Li Y., Lu L.;
RT "PLAB, a novel placental bone morphogenetic protein.";
RL Biochim. Biophys. Acta 1354:40-44(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=98256302; PubMed=9593718; DOI=10.1074/jbc.273.22.13760;
RA Paralkar V.M., Vail A.L., Grasser W.A., Brown T.A., Xu H., Vukicevic S., Ke H.Z., Qi H., Owen T.A., Thompson D.D.;
RT "Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family.";
RL J. Biol. Chem. 273:13760-13767(1998).
RN [5]
RP SEQUENCE OF 14-308 FROM N.A.
RX MEDLINE=98085971; PubMed=9426002; DOI=10.1016/S0378-1119(97)00485-X;
RA Lawton L.N., de Fatima Bonaldo M., Jelenc P.C., Qiu L., Baumes S.A., Marcelino R.A., de Jesus G.M., Wellington S., Knowles J.A.,

Q04906	rattus norv
Q9xyq7	lytechinus
P23359	mus musculus
O77681	ovis aries
P18075	homo sapien
O6pud1	anopheles g
Q7pzi7	anopheles g
Q6ha10	rattus norv
P22003	homo sapien
O96504	branchiosto
Q9ygh7	xenopus lae
O7t288	brachydanio
P49003	mus musculus
Q8cce0	mus musculus

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 25.703 Seconds
(without alignments)
1104.306 Million cell updates/sec

Title: US-10-009-431-3
Perfect score: 1550
Sequence: 1 MLVLVLSWLPHGALSLSA.....DTGVSLOTYYDLLAKDCHCI 295

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1522.5	98.2	309	2 JC5697	placental transfer
2	229	14.8	513	1 BMH06	bone morphogenetic
3	221	14.3	372	2 C39364	GDF-1 embryonic gr
4	216	13.9	510	2 A54798	Vg-1-related prote
5	215.5	13.9	365	2 T43286	cet-1 protein - Ca
6	212.5	13.7	402	2 A45056	osteogenic protein
7	212	13.7	354	2 S29718	gene nodal protein
8	208	13.4	207	2 S37618	vgr protein - rat
9	207	13.4	431	1 BMH07	bone morphogenetic
10	206.5	13.3	454	1 BMH05	bone morphogenetic
11	205	13.2	452	2 I49542	bone morphogenetic
12	204	13.2	360	2 A29619	Vgl embryonic grow
13	204	13.2	430	2 J01184	osteogenic protein
14	202	13.0	313	2 I51284	bone morphogenetic
15	199	12.8	455	2 A43918	TGF-beta-related p
16	196	12.6	426	2 JH0690	bone morphogenetic
17	193	12.5	350	2 JC5241	activin beta E cha
18	189.5	12.2	441	2 S45284	growth/differentia
19	188	12.1	398	2 JH0687	bone morphogenetic
20	187	12.1	357	2 A39364	GDF-1 embryonic gr
21	186.5	12.0	588	2 A26158	decapentaplegic pr
22	183	11.8	398	2 JH0688	bone morphogenetic
23	182.5	11.8	151	2 S43296	bone morphogenetic
24	179	11.5	393	2 S37073	bone morphogenetic
25	177	11.4	436	2 B55452	cartilage-derived
26	176	11.4	408	2 S58791	bone morphogenetic
27	175	11.3	501	2 JC2347	growth/differentia
28	174.5	11.3	476	2 JC4646	bone morphogenetic
29	174	11.2	461	2 S52408	SPDVR1 protein - s

30	173	11.2	501	2 A55452	cartilage-derived
31	172.5	11.1	408	2 S38343	bone morphogenetic
32	171	11.0	400	2 A49147	bone morphogenetic
33	171	11.0	401	2 JH0689	bone morphogenetic
34	171	11.0	495	2 S43294	bone morphogenetic
35	170	11.0	408	1 BMH04	bone morphogenetic
36	169.5	10.9	420	2 I49541	bone morphogenetic
37	169.5	10.9	478	2 JC4838	bone morphogenetic
38	168.5	10.9	366	2 A46607	growth/differentia
39	168	10.8	125	2 S43295	bone morphogenetic
40	167.5	10.8	394	2 S45355	bone morphogenetic
41	167	10.8	390	1 WFH02	transforming growt
42	167	10.7	390	2 A27512	transforming growt
43	166.5	10.7	391	2 S01413	transforming growt
44	166	10.7	352	2 JC2466	inhibin beta-C cha
45	165.5	10.7	373	2 A41918	transforming growt

ALIGNMENTS

RESULT 1

JC5697
placental transforming growth factor-beta homolog - human
C;Species: Homo sapiens (man)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5697
R;Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.
J. Biochem. 122, 622-626, 1997
A;Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in
A;Reference number: JC5697; MUID:98006316; PMID:9348093
A;Accession: JC5697
A;Molecule type: mRNA
A;Residues: 1-309 <YOK>
A;Cross-references: UNIPROT:Q9BWA0; DDBJ:AB000584
A;Experimental source: fibrosarcoma
C;Comment: This protein plays a role in reproduction.

Query Match 98.2%; Score 1522.5; DB 2; Length 309;
Best Local Similarity 99.0%; Pred. No. 1.1e-108;
Matches 293; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1	MLVLVLSWLPHGALSLSAASRASFPGPS-ELHTEDSPRELKREYEDLLTLRANQS	59
Db	14	MLVLVLSWLPHGALSLSAASRASFPGPS-ELHTEDSPRELKREYEDLLTLRANQS	73
Qy	60	WEDSNTDLVPAPAVRILTPVRLGSGGHLRLSRALPEGLPEASRLHRLPRLSPTAS	119
Db	74	WEDSNTDLVPAPAVRILTPVRLGSGGHLRLSRALPEGLPEASRLHRLPRLSPTAS	133
Qy	120	RSWDVTRPLRQLSLARPQAPALHRLSPPPSQSDQLAESSSARPOLEHLRPAARGR	179
Db	134	RSWDVTRPLRQLSLARPQAPALHRLSPPPSQSDQLAESSSARPOLEHLRPAARGR	193
Qy	180	RRARANGDHCPGRCRCRLHTVRASLEDLGHADWVLSPREVQVTWCIGACSPQFAAN	239
Db	194	RRARANGDHCPGRCRCRLHTVRASLEDLGHADWVLSPREVQVTWCIGACSPQFAAN	253
Qy	240	MHAQIKTSLHRLKPDTPVAPCCVPASYNPMVLQKTDGTGVSLOTYYDLLAKDCHCI	295
Db	254	MHAQIKTSLHRLKPDTPVAPCCVPASYNPMVLQKTDGTGVSLOTYYDLLAKDCHCI	309

RESULT 2

BMH06
bone morphogenetic protein 6 precursor - human
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: B39263
R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Wang, E.A.; Woz
Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A;Title: Identification of transforming growth factor beta family members present in bo
A;Reference number: A39263; MUID:91088608; PMID:2263636

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:44:20 ; Search time 99.8911 Seconds
(without alignments)
1142.187 Million cell updates/sec

Title: US-10-009-431-3

Perfect score:

Sequence: 1 MLLVLLVLSWLPHGGLSLA.....DTGVSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

[illegible]

searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*

```
1: _ geneseqp1980s:*
```

2: geneseq1990s:*

3: geneseqp2000s:*

```
4: geneseqp20018:*
5: geneseqm20028:*
```

6: [geneseqp2003as:*](#)

7: [geneseqp2003bs:*](#)

8: **geneseqp20048:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1550	100.0	295	4	AAB36557	Aab36557 Human GDF
2	1550	100.0	308	2	AAR77097	Aar77097 Human TGF
3	1550	100.0	308	2	AAW10662	Aaw10662 Human TGF
4	1550	100.0	308	3	AAB36132	Aab36132 Human TGF
5	1550	100.0	308	5	ABB09174	Abb09174 Human TGF
6	1550	100.0	308	5	AAE13538	Aae13538 Human TGF
7	1550	100.0	308	6	ADAI1070	Adai1070 Human mac
8	1550	100.0	308	8	ADe77027	Ad77027 Human pro
9	1550	100.0	308	8	ADL12720	Adl12720 Human ste
10	1546	99.7	308	2	AAR84710	Aar84710 Human emb
11	1546	99.7	308	2	AAW10673	Aaw10673 Human TGF
12	1546	99.7	308	2	AAW10666	Aaw10666 Human TGF
13	1546	99.7	308	2	AAW10672	Aaw10672 Human TGF
14	1546	99.7	308	2	AAW10668	Aaw10668 Human TGF
15	1546	99.7	308	2	AAW10667	Aaw10667 Human TGF
16	1546	99.7	308	2	AAW10671	Aaw10671 Human TGF
17	1546	99.7	308	2	AAW48672	Aaw48672 GF-2H pro
18	1546	99.7	308	7	ADI63071	Adi63071 Human apo
19	1546	99.7	308	8	ABM82070	Abm82070 Tumour-as
20	1542	99.5	308	8	ADG71946	Adg71946 Human NOV
21	1542	99.5	308	8	ADJ87283	Adj87283 Human G p
22	1538	99.2	295	2	AAW02613	Aaw02613 Human pro
23	1537	99.2	308	2	AAW10670	Aaw10670 Human TGF
24	1537	99.2	308	2	AAW10669	Aaw10669 Human TGF
25	1537	99.2	308	5	AAE13539	Aae13539 Human mac

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:47:41 ; Search time 11.7545 Seconds
(without alignments)
711.279 Million cell updates/sec

Title: US-10-009-431-4
Perfect score: 624
Sequence: 1 ARNGDHCPGRCRLHTV.....DTGVSQTYDILLAKDCHCI 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	112	3	US-08-927-433-8
2	624	100.0	112	3	US-08-927-433-10
3	624	100.0	119	4	US-08-626-185-4
4	624	100.0	308	3	US-08-927-433-9
5	624	100.0	308	3	US-08-775-882-4
6	624	100.0	308	3	US-08-775-882-6
7	624	100.0	308	4	US-09-276-600-6
8	624	100.0	308	4	US-09-976-594-449
9	624	100.0	308	4	US-09-919-039-192
10	624	100.0	314	4	US-09-949-016-10118
11	620	99.4	295	2	US-08-411-607A-2
12	620	99.4	295	4	US-09-361-741-2
13	620	99.4	295	4	US-09-461-418-2
14	609	97.6	308	4	US-09-949-016-6559
15	545	87.3	99	3	US-08-775-882-2
16	456	73.1	115	4	US-09-463-931-2
17	201	32.2	36	4	US-09-276-600-7
18	196	31.4	117	4	US-09-374-958C-69
19	196	31.4	139	4	US-09-374-958C-68
20	195	31.2	118	1	US-08-481-377-14
21	195	31.2	118	2	US-08-491-835-12
22	195	31.2	118	3	US-09-153-733A-14
23	195	31.2	118	3	US-08-946-092A-12
24	195	31.2	118	3	US-09-172-062-12
25	195	31.2	118	3	US-09-301-520D-12
26	195	31.2	118	3	US-09-389-705-14
27	195	31.2	118	5	PCT-US94-006666-14

28 195 31.2 118 5 PCT-US94-00685-12 Sequence 12, Appl
29 195 31.2 438 2 US-08-459-346-14 Sequence 14, Appl
30 195 31.2 438 3 US-08-889-419-14 Sequence 14, Appl
31 195 31.2 438 3 US-08-402-542-14 Sequence 14, Appl
32 195 31.2 438 5 PCT-US93-07189-14 Sequence 14, Appl
33 195 31.2 455 1 US-08-278-729A-25 Sequence 25, Appl
34 195 31.2 455 1 US-08-155-343A-25 Sequence 25, Appl
35 195 31.2 455 1 US-08-406-672-25 Sequence 25, Appl
36 195 31.2 455 1 US-08-643-563A-25 Sequence 25, Appl
37 195 31.2 455 1 US-08-643-763A-25 Sequence 25, Appl
38 195 31.2 455 1 US-08-462-623-25 Sequence 25, Appl
39 195 31.2 455 1 US-08-451-953A-25 Sequence 25, Appl
40 195 31.2 455 2 US-08-459-346-16 Sequence 16, Appl
41 195 31.2 455 2 US-08-445-468A-25 Sequence 25, Appl
42 195 31.2 455 2 US-08-461-397A-25 Sequence 25, Appl
43 195 31.2 455 3 US-08-912-088-25 Sequence 25, Appl
44 195 31.2 455 3 US-08-278-730A-25 Sequence 25, Appl
45 195 31.2 455 3 US-08-889-419-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-927-433-8
; Sequence 8, Application US/08927433
; Patent No. 6107476
; GENERAL INFORMATION:
; APPLICANT: Erlander, Mark G.
; APPLICANT: Huang, Shaoming
; APPLICANT: Jackson, Michael A.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND RELA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One J & J Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/927,433
; APPLICATION NUMBER: US/08/927,433
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrison, Alan J.
; REGISTRATION NUMBER: 37,399
; REFERENCE/DOCKET NUMBER: ORT-849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-3592
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-927-433-8

Query Match 100.0%; Score 624; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.3e-64;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARNGDHCPGRCRLHTVRASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANHAQ 60
Db 1 ARNGDHCPGRCRLHTVRASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANHAQ 60

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:49:12 ; Search time 32.3802 Seconds
(without alignments)
1245.908 Million cell updates/sec

Title: US-10-009-431-4
Perfect score: 624
Sequence: 1 ARNGDHCPLGRCRRLTV.....DTGVSLQTYDILLADCHCI 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	119	US-10-373-581-4	Sequence 4, Appli
2	624	100.0	283	US-10-211-689-76	Sequence 76, Appl
3	624	100.0	308	US-09-276-600-6	Sequence 6, Appli
4	624	100.0	308	US-09-981-353-188	Sequence 188, App
5	624	100.0	308	US-09-919-039-192	Sequence 192, App
6	624	100.0	308	US-10-000-628-6	Sequence 6, Appli
7	624	100.0	308	US-10-257-597-2	Sequence 2, Appli
8	624	100.0	308	US-10-425-115-229584	Sequence 229584,
9	620	99.4	295	US-09-361-741-2	Sequence 2, Appli
10	620	99.4	295	US-10-270-377-2	Sequence 2, Appli
11	616	98.7	308	US-10-211-689-72	Sequence 72, Appl
12	615	98.6	308	US-10-257-597-1	Sequence 1, Appli

```
13 609 97.6 308 14 US-10-205-823-327 Sequence 327, App
14 609 97.6 308 14 US-10-021-660-113 Sequence 113, App
15 609 97.6 308 14 US-10-295-027-618 Sequence 618, App
16 609 97.6 308 15 US-10-295-027-1379 Sequence 1379, Ap
17 609 97.6 308 15 US-10-211-462-191 Sequence 191, App
18 609 97.6 308 16 US-10-448-664-2 Sequence 2, Appli
19 540 86.5 102 15 US-10-211-689-74 Sequence 74, Appli
20 456 73.1 115 14 US-10-194-382-2 Sequence 68, Appli
21 431 69.1 298 9 US-09-789-919-68 Sequence 76, App
22 244 39.1 45 16 US-10-408-765A-976 Sequence 77, Appl
23 205 32.9 102 11 US-09-930-512-77 Sequence 210, App
24 205 32.9 102 15 US-10-080-334-210 Sequence 300, App
25 205 32.9 102 15 US-10-074-978A-300 Sequence 831, App
26 205 32.9 102 15 US-10-072-012-831 Sequence 833, App
27 205 32.9 102 15 US-10-072-012-833 Sequence 7, Appli
28 201 32.2 36 9 US-09-276-600-7 Sequence 7, Appli
29 201 32.2 36 13 US-10-000-628-7 Sequence 14, Appli
30 195 31.2 118 9 US-09-389-705-14 Sequence 12, Appli
31 195 31.2 118 13 US-10-115-406-12 Sequence 14, Appli
32 195 31.2 118 14 US-10-154-333-14 Sequence 14, Appli
33 195 31.2 118 16 US-10-704-223-12 Sequence 12, Appli
34 195 31.2 438 14 US-10-122-026-14 Sequence 14, Appli
35 195 31.2 455 8 US-08-260-675-25 Sequence 25, Appli
36 195 31.2 455 10 US-09-952-318A-25 Sequence 25, Appli
37 195 31.2 455 14 US-10-122-026-16 Sequence 16, Appli
38 195 31.2 455 14 US-10-050-050-25 Sequence 25, Appli
39 194 31.1 430 8 US-08-260-675-19 Sequence 19, Appli
40 194 31.1 430 16 US-10-385-064-16 Sequence 16, Appli
41 192 30.8 118 9 US-09-389-705-11 Sequence 11, Appli
42 192 30.8 118 14 US-10-154-333-11 Sequence 11, Appli
43 192 30.8 139 8 US-08-260-675-6 Sequence 6, Appli
44 192 30.8 139 10 US-09-952-318A-6 Sequence 6, Appli
45 192 30.8 139 14 US-10-050-050-6 Sequence 6, Appli
```

ALIGNMENTS

RESULT 1

```
US-10-373-581-4
; Sequence 4, Application US/10373581
; Publication No. US20030211541A1
; GENERAL INFORMATION:
; APPLICANT: Lee et al., Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-14
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,581
; FILING DATE: 24-Feb-2003
; CLASSIFICATION DATA:
; APPLICATION NUMBER: US/08/626,185
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:10 ; Search time 34.1545 Seconds
(without alignments)
1679.221 Million cell updates/sec

Title: US-10-009-431-4

Perfect score: 624

Sequence: 1 ARNGDHCPLGPGRCRLHTV.....DTGVSLQTYDDLLAKDCHCI 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	308	1	GDFF_HUMAN
2	624	100.0	308	2	Q9BWA0
3	456	73.1	303	1	GDFF_MOUSE
4	456	73.1	303	2	Q6NX63
5	448	71.8	303	1	GDFF_RAT
6	249	39.9	387	2	Q869H8
7	204	32.7	373	2	Q90723
8	204	32.7	373	2	Q98950
9	201	32.2	365	2	O02424
10	201	32.2	365	2	O76514
11	201	32.2	424	2	O6PA74
12	198	31.7	288	2	Q6PUB1
13	197.5	31.7	350	2	Q66KL4
14	197	31.6	441	2	Q6PUD1
15	197	31.6	441	2	Q7P217
16	195	31.2	455	1	60A_DROME
17	194.5	31.2	354	2	Q9YGV1
18	193	30.9	424	2	Q9YGH7
19	192	30.8	430	1	BMP7_MOUSE
20	191	30.6	436	1	60A_DROVI
21	191	30.6	446	2	Q7T288
22	191	30.6	513	1	BMP6_HUMAN
23	190	30.4	426	1	BMP7_XENLA
24	190	30.4	426	2	Q6PFF5
25	188	30.1	207	1	BMP6_RAT
26	188	30.1	313	2	Q91403
27	188	30.1	398	2	Q918T6
28	188	30.1	424	2	Q6P2B8
29	188	30.1	431	1	BMP7_HUMAN
30	188	30.1	435	2	Q8BRW3
31	188	30.1	452	1	BMP5_MOUSE

32	188	30.1	453	2	P87373	P87373	gallus gall
33	188	30.1	454	1	BMP5_HUMAN	P22003	homo sapien
34	188	30.1	454	2	Q8CCE0	Q8CCE0	mus musculus
35	188	30.1	506	2	Q811S4	Q811S4	rattus norv
36	188	30.1	510	1	BMP6_MOUSE	P20722	mus musculus
37	187	30.0	355	1	DVR1_BRARE	P35621	brachydanio
38	185	29.6	356	2	Q7T2G5	Q7T2G5	xenopus bor
39	185	29.6	360	1	DVR1_XENLA	P09534	xenopus lae
40	184	29.5	432	2	Q9PTF9	Q9PTF9	brachydanio
41	182	29.2	444	2	Q6GUA6	Q6GUA6	sus scrofa
42	182	29.2	453	1	GDF9_CAPHI	O66nc0	capra hircu
43	182	29.2	453	1	GDF9_SHEEP	O77681	ovis aries
44	181	29.0	444	2	Q6DOX1	Q6dql1	sus scrofa
45	180.5	28.9	382	2	Q8HY13	Q8hy13	trichosurus

ALIGNMENTS

RESULT 1
ID GDFF_HUMAN STANDARD; PRT; 308 AA.
AC Q99988; O14629; P78360; Q9NRT0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 44, Last sequence update)
DE Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1).
DE Name=GDF15; Synonyms=MIC1, PDF, PLAB, PTGFB;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=98006316; PubMed=9348093;
RA Yokoyama-Kobayashi M., Saeki M., Sekine S., Kato S.;
RT "Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in placenta."
RL J. Biochem. 122:622-626(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97470998; PubMed=9326641; DOI=10.1073/pnas.94.21.11514;
RX Bootcov M.R., Bauekin A.R., Valenzuela S.M., Moore A.G., Bansal M., He X.Y., Zhang H.P., Donnellan M., Mahler S., Pryor K., Walsh B.J., Nicholson R.C., Fairlie W.D., For S.B., Robbins J.M., Breit S.N.;
RA "MIC-1, a novel macrophage inhibitory cytokine, is a divergent member of the TGF-beta superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:11514-11519(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98041637; PubMed=9375789; DOI=10.1016/S0167-4781(97)00122-X;
RA Hromas R., Hufford M., Sutton J., Xu D., Li Y., Lu L.;
RT "PLAB, a novel placental bone morphogenetic protein."
RL Biochim. Biophys. Acta 1354:40-44(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98256302; PubMed=9593718; DOI=10.1074/jbc.273.22.13760;
RA Paralkar V.M., Vail A.L., Grasser W.A., Brown T.A., Xu H., Vukicevic S., Ke H.Z., Qi H., Owen T.A., Thompson D.D.;
RT "Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family."
RL J. Biol. Chem. 273:13760-13767(1998).
RN [5]
RP SEQUENCE OF 14-308 FROM N.A.
RX MEDLINE=98085971; PubMed=9426002; DOI=10.1016/S0378-1119(97)00485-X;
RA Lawton L.N., de Fatima Bonaudo M., Jelenc P.C., Giu L., Baumes S.A., Marcelino R.A., de Jesus G.M., Wellington S., Knowles J.A.,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 9.75842 Seconds
(without alignments)
1104.306 Million cell updates/sec

Title: US-10-009-431-4
Perfect score: 624
Sequence: 1 ARNGDHCPLGPRCCRLHTV.....DTGVSLOTYYDILLAKDCHCI 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	309	2 JC5697	placental transfer
2	201	32.2	365	2 T43286	Cet-1 protein - Ca
3	195	31.2	455	2 A43918	TGF-beta-related p
4	192	30.8	430	2 JQ1184	osteogenic protein
5	191	30.6	513	1 BMH06	bone morphogenetic
6	190	30.4	426	2 JH0690	bone morphogenetic
7	188	30.1	207	2 S37618	vgr protein - rat
8	188	30.1	313	2 I51284	bone morphogenetic
9	188	30.1	431	1 BMH07	bone morphogenetic
10	188	30.1	452	2 I49542	bone morphogenetic
11	188	30.1	454	1 BMH05	bone morphogenetic
12	188	30.1	510	2 A54798	Vg-1-related prote
13	185	29.6	360	2 A29619	Vg1 embryonic grow
14	179.5	28.8	151	2 S43296	bone morphogenetic
15	176	28.2	372	2 C39364	GFP-1 embryonic gr
16	175	28.0	402	2 A45056	osteogenic protein
17	174	27.9	441	2 S45284	growth/differentia
18	170	27.2	588	2 A26158	decapentaplegic pr
19	169.5	27.2	495	2 S43296	bone morphogenetic
20	169.5	27.2	501	2 JC2347	growth/differentia
21	169.5	27.2	501	2 A55452	cartilage-derived
22	167	26.8	354	2 S29718	gene nodal protein
23	165	26.4	461	2 S52408	SPDV1 protein - s
24	163.5	26.2	125	2 S43295	bone morphogenetic
25	163	26.1	357	2 A39364	GDF-1 embryonic gr
26	162.5	26.0	366	2 A46607	growth/differentia
27	157.5	25.2	366	2 A45402	transforming growt
28	156	25.0	436	2 B55452	cartilage-derived
29	150.5	24.1	350	2 JC5241	activin beta E cha

30	150.5	24.1	476	2 JC4646	bone morphogenetic
31	149	23.9	472	1 BMH03	bone morphogenetic
32	148.5	23.8	401	2 JH0689	bone morphogenetic
33	148	23.7	360	2 I53032	bone morphogenetic
34	147.5	23.6	352	2 JC2466	inhibin beta-C cha
35	147.5	23.6	400	2 A49147	bone morphogenetic
36	147.5	23.6	408	1 BMH04	bone morphogenetic
37	147.5	23.6	408	2 S58791	bone morphogenetic
38	147.5	23.6	408	2 S38343	bone morphogenetic
39	147.5	23.6	420	2 I49541	bone morphogenetic
40	147.5	23.6	427	2 A40735	TGF beta homolog d
41	147.5	23.6	478	2 J48338	bone morphogenetic
42	146.5	23.5	405	2 I50608	bone morphogenetic
43	145.5	23.3	373	2 PW0042	activin - fruit fl
44	143.5	23.0	367	2 JC4151	activin beta-D cha
45	143.5	23.0	398	2 JH0688	bone morphogenetic

ALIGNMENTS

RESULT 1

JC5697
placental transforming growth factor-beta homolog - human
C;Species: Homo sapiens (man)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5697
R;Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.
J. Biochem. 122, 622-626, 1997
A;Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in
A;Reference number: JC5697; MUID:98006316; PMID:9348093
A;Accession: JC5697
A;Molecule type: mRNA
A;Residues: 1-309 <YOK>
A;Cross-references: UNIPROT:Q9BWA0; DDBJ:AB0000584
A;Experimental source: fibrosarcoma
C;Comment: This protein plays a role in reproduction.

Query Match 100.0%; Score 624; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.3e-55;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ARNGDHCPLGPRCCRLHTV	ASLEDLGWADWVLSPREVQV	TMCTGICACPSQFRAAN	HAQ 60
DB	198	ARNGDHCPLGPRCCRLHTV	ASLEDLGWADWVLSPREVQV	TMCTGICACPSQFRAAN	HAQ 257
QY	61	IKTSLHRLKPDTPAPCCVP	ASYNPMVLIQKTDGVSLOT	YYDILLAKDCHCI 112	
DB	258	IKTSLHRLKPDTPAPCCVP	ASYNPMVLIQKTDGVSLOT	YYDILLAKDCHCI 309	

RESULT 2

T43286
Cet-1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43286
R;Morita, K.; Chow, K.L.; Ueno, N.
Development 126, 1337-1347, 1999
A;Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis
A;Reference number: 222393; MUID:99146896; PMID:10021351
A;Accession: T43286
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <MOR>
A;Cross-references: UNIPROT:O76514; EMBL:AF074395; NID:G3328181; PIDN:AAC26791.1; PID:8
C;Genetics:
A;Gene: cet-1
A;Map position: 5
C;Superfamily: inhibin

Query Match 32.2%; Score 201; DB 2; Length 365;
Best Local Similarity 36.3%; Pred. No. 1e-12;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:29:15 ; Search time 72 Seconds
(without alignments)
601.627 Million cell updates/sec

Title: US-10-009-431-4

Perfect score: 624
Sequence: 1. ARNGDHCPGRCRLHTV.....DTGVSLOTYDILLAKDCHCI 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	112	2	AAR84709 Human emb
2	624	100.0	112	2	AAB36558 Human GDP
3	624	100.0	119	2	AAW31509 Growth di
4	624	100.0	141	2	AAW10674 TGF-beta-
5	624	100.0	154	2	AAW10665 Human TGF
6	624	100.0	203	2	AAW10664 Human TGF
7	624	100.0	283	8	ADJ87287 Human G p
8	624	100.0	295	4	AAB36557 Human GDP
9	624	100.0	308	2	AAR77097 Human TGF
10	624	100.0	308	2	AAR84710 Human emb
11	624	100.0	308	2	AAW10673 Human TGF
12	624	100.0	308	2	AAW10666 Human TGF
13	624	100.0	308	2	AAW10672 Human TGF
14	624	100.0	308	2	AAW10662 Human TGF
15	624	100.0	308	2	AAW10668 Human TGF
16	624	100.0	308	2	AAW10667 Human TGF
17	624	100.0	308	2	AAW10671 Human TGF
18	624	100.0	308	2	AAW48672 GF-2H pro
19	624	100.0	308	3	AAB26122 Human TGF
20	624	100.0	308	5	ABB09174 Human NAG
21	624	100.0	308	5	AAE13538 Human mac
22	624	100.0	308	6	ADA11070 Human cdn
23	624	100.0	308	7	ADI63071 Human apo
24	624	100.0	308	8	ADE77027 Human pro
25	624	100.0	308	8	ADL12720 Human ste

ALIGNMENTS

RESULT 1

AAR84709

ID AAR84709 standard; protein; 112 AA.

XX AAR84709;

XX 23-MAY-1996 (first entry)

XX Human embryonal lung mature protein.

XX Eosinophil; inhibitor; active oxygen production; bronchial asthma; human; embryonal lung.

XX Homo sapiens.

XX JF07258293-A.

XX 09-OCT-1995.

XX 23-MAR-1994; 94JP-00052225.

XX 23-MAR-1994; 94JP-00052225.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1995-380074/49.

XX N-PSDB; AAT05177.

XX A new protein for the treatment of bronchial asthma - inhibits the production of active oxygen in eosinophil(s).

XX Claim 1; Page 2; 26pp; Japanese.

XX The present sequence is that of a 112 amino acid mature protein isolated from normal diploid cells of human embryonal lung tissue. The protein inhibits production of active oxygen in eosinophils and is useful for treatment and prevention of bronchial asthma

XX Sequence 112 AA;

Query Match 100.0%; Score 624; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 4e-57;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNGDHCPGRCRLHTVTRASLEDLGNADWVLSPREVQVTMCIGACPSQFRAANHAQ 60

Db 1 ARNGDHCPGRCRLHTVTRASLEDLGNADWVLSPREVQVTMCIGACPSQFRAANHAQ 60

Abm82070 Tumour-as
Aaw10663 Human TGF
Aaw02613 Human pro
Adg71946 Human NOV
Adj87283 Human G p
Aaw10670 Human TGF
Aaw10669 Human TGF
Aae13539 Human mac
Adr66910 Human pro
Adr66012 Human pro
Abo03550 Angiogene
Abo56743 Lung can
Adb75503 Prostate
Adn39300 Cancer/an
Adn40061 Cancer/an
Adp25261 PRO polyp
Adg71948 Human NOV
Adj87285 Human G p
Aar77096 Human TGF
Aaw93161 Murine GD

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:47:41 ; Search time 10.2851 Seconds
(without alignments)
711.279 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111
Perfect score: 541
Sequence: 1 CCRHTVRASLELDGWADWV.....TDTGVSLSQTYDDLLAKDCHC 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	99	3	US-08-775-882-2
2	541	100.0	112	3	US-08-927-433-8
3	541	100.0	112	3	US-08-927-433-10
4	541	100.0	119	4	US-08-626-185-4
5	541	100.0	308	3	US-08-927-433-9
6	541	100.0	308	3	US-08-775-882-4
7	541	100.0	308	3	US-08-775-882-6
8	541	100.0	308	4	US-03-276-600-6
9	541	100.0	308	4	US-03-976-594-449
10	541	100.0	308	4	US-03-919-039-192
11	541	100.0	314	4	US-03-949-016-10118
12	537	99.3	295	2	US-08-411-607A-2
13	537	99.3	295	4	US-03-361-741-2
14	537	99.3	295	4	US-03-461-418-2
15	535	98.9	308	4	US-03-949-016-6559
16	407	75.2	115	4	US-09-463-931-2
17	195	36.0	117	4	US-09-374-958C-69
18	195	36.0	139	4	US-09-374-958C-68
19	195	36.0	438	2	US-08-459-346-14
20	195	36.0	438	3	US-08-889-419-14
21	195	36.0	438	3	US-08-402-542-14
22	195	36.0	438	5	PCT-US93-07189-14
23	193	35.7	102	4	US-09-374-958C-53
24	193	35.7	430	1	US-07-841-646-25
25	193	35.7	430	1	US-07-901-703-9
26	193	35.7	430	3	US-08-445-467-19
27	193	35.7	430	4	US-09-464-206-16

28	193	35.7	430	4	US-08-404-113A-16	Sequence 16, Appl
29	193	35.7	430	4	US-08-260-675-19	Sequence 19, Appl
30	193	35.7	430	5	PCT-US90-07654-2	Sequence 2, Appli
31	193	35.7	430	5	PCT-US92-01968-19	Sequence 19, Appl
32	193	35.7	430	5	PCT-US93-05446-9	Sequence 9, Appli
33	193	35.7	430	5	PCT-US93-07190-19	Sequence 19, Appl
34	193	35.7	430	5	PCT-US93-07231-19	Sequence 19, Appl
35	193	35.7	430	5	PCT-US93-08742-19	Sequence 19, Appl
36	193	35.7	430	5	PCT-US93-08808-19	Sequence 19, Appl
37	193	35.7	430	5	PCT-US93-08885-19	Sequence 19, Appl
38	193	35.7	430	5	PCT-US93-10520-6	Sequence 6, Appli
39	192	35.5	118	1	US-08-481-377-11	Sequence 11, Appl
40	192	35.5	118	3	US-09-153-733A-11	Sequence 11, Appl
41	192	35.5	118	3	US-09-389-705-11	Sequence 11, Appl
42	192	35.5	118	5	PCT-US94-00666-11	Sequence 11, Appl
43	191	35.3	102	2	US-08-288-508C-17	Sequence 17, Appl
44	191	35.3	102	3	US-08-478-097A-14	Sequence 14, Appl
45	191	35.3	102	3	US-08-289-222E-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-775-882-2
; Sequence 2, Application US/08775882
; Patent No. 6180602
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: OH, Suwan
; APPLICANT: SEKINE, Shingo
; APPLICANT: SAKI, Minoru
; APPLICANT: KOBAYASHI, Midori
; APPLICANT: YADA, Mika
; APPLICANT: TSUJI, Tomoko
; APPLICANT: OHMORI, Hitoshi
; TITLE OF INVENTION: HUMAN NOVEL CDNA, TGF-BETA SUPERFAMILY
; TITLE OF INVENTION: PROTEIN ENCODED THEREBY AND THE USE AS IMMUNOSUPPRESSIVE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,882
; FILING DATE: 02-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390,207
; FILING DATE: 16-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,441
; FILING DATE: 03-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-61431
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-327619
; FILING DATE: 13-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-208077
; FILING DATE: 04-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:49:12 ; Search time 28.3327 Seconds
(without alignments)
1245.908 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111

Perfect score: 541

Sequence: 1 CCEHHTVRASLEGLGWADWV.....TTGVSLQTYDILLAKDCHC 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	119	15	US-10-373-581-4
2	541	100.0	283	15	US-10-211-689-76
3	541	100.0	308	9	US-09-276-600-6
4	541	100.0	308	9	US-09-981-353-188
5	541	100.0	308	10	US-09-919-039-192
6	541	100.0	308	13	US-10-000-628-6
7	541	100.0	308	15	US-10-257-597-1
8	541	100.0	308	16	US-10-425-597-2
9	541	100.0	308	16	US-10-425-597-2
10	537	99.3	295	9	US-09-361-741-2
11	537	99.3	295	14	US-10-270-377-2
12	535	98.9	308	14	US-10-205-823-327
					Sequence 4, Appli
					Sequence 618, App
					Sequence 1379, Ap
					Sequence 191, Appli
					Sequence 2, Appli
					Sequence 72, Appli
					Sequence 74, Appli
					Sequence 2, Appli
					Sequence 68, Appli
					Sequence 976, App
					Sequence 77, Appli
					Sequence 210, App
					Sequence 300, App
					Sequence 831, App
					Sequence 833, App
					Sequence 14, Appli
					Sequence 19, Appli
					Sequence 16, Appli
					Sequence 11, Appli
					Sequence 28, Appli
					Sequence 14, Appli
					Sequence 9, Appli
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 62, Appli
					Sequence 6, Appli
					Sequence 5, Appli
					Sequence 25, Appli
					Sequence 19, Appli
					Sequence 4, Appli

13 535 98.9 308 14 US-10-021-660-113 Sequence 113, App
14 535 98.9 308 15 US-10-295-027-618 Sequence 618, App
15 535 98.9 308 15 US-10-295-027-1379 Sequence 1379, Ap
16 535 98.9 308 16 US-10-211-462-191 Sequence 191, Appli
17 535 98.9 308 16 US-10-448-664-2 Sequence 2, Appli
18 533 98.5 308 15 US-10-211-689-72 Sequence 72, Appli
19 532 98.3 102 15 US-10-211-689-74 " Sequence 74, Appli
20 407 75.2 115 14 US-10-194-382-2 Sequence 2, Appli
21 382 70.6 298 9 US-09-789-919-68 Sequence 68, Appli
22 240 44.4 45 16 US-10-408-765A-976 Sequence 976, App
23 205 37.9 102 11 US-09-930-512-77 Sequence 77, Appli
24 205 37.9 102 15 US-10-080-334-210 Sequence 210, App
25 205 37.9 102 15 US-10-074-978A-300 Sequence 300, App
26 205 37.9 102 15 US-10-072-012-831 Sequence 831, App
27 205 37.9 102 15 US-10-072-012-833 Sequence 833, App
28 195 36.0 438 14 US-10-122-026-14 Sequence 14, Appli
29 193 35.7 430 8 US-08-260-675-19 Sequence 19, Appli
30 193 35.7 430 16 US-10-385-064-16 Sequence 16, Appli
31 192 35.5 118 9 US-09-389-708-11 Sequence 11, Appli
32 192 35.5 118 14 US-10-154-333-11 Sequence 11, Appli
33 191 35.3 102 10 US-09-952-318A-6 Sequence 28, Appli
34 191 35.3 102 14 US-10-187-394-14 Sequence 14, Appli
35 191 35.3 118 13 US-10-115-406-9 Sequence 9, Appli
36 191 35.3 118 16 US-10-704-223-9 Sequence 9, Appli
37 191 35.3 139 8 US-08-260-675-6 Sequence 6, Appli
38 191 35.3 139 10 US-09-952-318A-6 Sequence 6, Appli
39 191 35.3 139 14 US-10-050-050-6 Sequence 6, Appli
40 191 35.3 139 15 US-10-366-345-62 Sequence 62, Appli
41 191 35.3 139 16 US-10-385-064-6 Sequence 6, Appli
42 191 35.3 143 13 US-10-002-278-5 Sequence 5, Appli
43 191 35.3 430 8 US-08-957-425-25 Sequence 25, Appli
44 191 35.3 430 10 US-09-952-318A-19 Sequence 19, Appli
45 191 35.3 430 14 US-10-122-026-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-373-581-4
; Sequence 4, Application US/10373581
; Publication No. US20030211541A1
; GENERAL INFORMATION:
; APPLICANT: Lee et al., Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-14
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/373,581
; FILING DATE: 24-Feb-2003
; CLASSIFICATION: 536
; APPLICATION NUMBER: US/08/626,185
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:10 ; Search time 29.8851 Seconds
(without alignments)
1679.221 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111

Perfect score: 541

Sequence: 1 CRLHTVRASLEDLGWADWV.....TDGTGVSLOTYDDLAKDCHC 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	541	100.0	308	1	GDFF_HUMAN	Q99888 homo sapien
2	541	100.0	308	1	Q9BWA0	Q9BWA0 homo sapien
3	407	75.2	303	1	GDFF_MOUSE	Q92017 mus musculus
4	407	75.2	303	2	Q6NXG3	Q6NXG3 mus musculus
5	399	73.8	303	1	GDFF_RAT	Q92016 rattus norv
6	239	44.2	387	2	Q869F8	Q869H8 crassostrea
7	201	37.2	365	2	Q02424	Q02424 caenorhabdi
8	201	37.2	365	2	Q76514	Q76514 caenorhabdi
9	200	37.0	424	2	Q6P4J4	Q6P4J4 xenopus tro
10	195	36.0	288	2	Q6PUB1	Q6PUB1 anopheles s
11	194	35.9	441	2	Q6PUD1	Q6PUD1 anopheles s
12	194	35.9	441	2	Q7PZ17	Q7PZ17 anopheles g
13	192	35.5	424	2	Q9YGH7	Q9YGH7 xenopus lae
14	191	35.3	430	1	BMP7_MOUSE	P23359 mus musculus
15	191	35.3	513	1	BMP6_HUMAN	P22004 homo sapien
16	189	34.9	373	2	Q90723	Q90723 gallus gall
17	189	34.9	373	2	Q98950	Q98950 gallus gall
18	188	34.8	207	1	BMP6_RAT	Q04906 rattus norv
19	188	34.8	350	2	Q66KL4	Q66KL4 xenopus tro
20	188	34.8	426	1	BMP7_XENLA	P30886 xenopus lae
21	188	34.8	426	2	Q6PF75	Q6PF75 xenopus lae
22	188	34.8	435	2	Q8BRW3	Q8BRW3 mus musculus
23	188	34.8	506	2	Q811S4	Q811S4 rattus norv
24	188	34.8	510	1	BMP6_MOUSE	P20742 mus musculus
25	187	34.6	313	2	Q914D3	Q914D3 gallus gall
26	187	34.6	398	2	Q918T6	Q918T6 gallus gall
27	187	34.6	424	2	Q6F2B8	Q6F2B8 xenopus tro
28	187	34.6	431	1	BMP7_HUMAN	P18075 homo sapien
29	187	34.6	436	1	60A_DROVI	Q24735 drosophila
30	187	34.6	455	1	60A_DROME	P27091 drosophila
31	186	34.4	446	2	Q7T288	Q7T288 brachydanio

32	185	34.2	354	2	Q9YGV1	Q9YGV1 xenopus lae
33	184	34.0	452	1	BMP5_MOUSE	P49003 mus musculus
34	184	34.0	453	2	P87373	P87373 gallus gall
35	184	34.0	454	1	BMP5_HUMAN	P22003 homo sapien
36	184	34.0	454	2	Q8CCE0	Q8CCE0 mus musculus
37	181	33.5	356	2	Q7T2G5	Q7T2G5 xenopus bor
38	181	33.5	360	1	DVR1_XENLA	P09534 xenopus lae
39	180	33.3	382	2	Q8HYI3	Q8HYI3 trichosurus
40	180	33.3	432	2	Q9PTF9	Q9PTF9 brachydanio
41	180	33.3	444	2	Q6DQX1	Q6DQX1 sus scrofa
42	180	33.3	444	2	Q6GUA6	Q6GUA6 sus scrofa
43	180	33.3	453	1	GDF9_CAPHI	Q66nc0 capra hircu
44	180	33.3	453	1	GDF9_SHEEP	O77681 ovis aries
45	178	32.9	453	2	Q9GK68	Q9GK68 bos taurus

ALIGNMENTS

RESULT 1

ID GDFF_HUMAN STANDARD; PRT; 308 AA.
AC Q99888; O14629; P78360; Q9NRTO;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)
DE Names=GDF15; Synonyms=MIC1, PDF, PLAB, PTGFB;
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=98006316; PubMed=9348093;
RA Yokoyama-Kobayashi M., Saeki M., Sekine S., Kato S.;
RT "Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in placenta.";
RL J. Biochem. 122:622-626(1997).
[2]
RN SEQUENCE FROM N.A.
RC MEDLINE=97470998; PubMed=9326641; DOI=10.1073/pnas.94.21.11514;
RX Bootcov M.R., Bauekin A.R., Valenzuela S.M., Moore A.G., Bansal M., He X.Y., Zhang H.P., Domellian M., Mahler S., Pryor K., Walsh B.J., Nicholson R.C., Fairlie W.D., Por S.B., Robbins J.M., Breit S.N.;
RT "MIC-1, a novel macrophage inhibitory cytokine, is a divergent member of the TGF-beta superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11514-11519(1997).
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98041637; PubMed=9375789; DOI=10.1016/S0167-4781(97)00122-X;
RA Thomas R., Hufford M., Sutton J., Xu D., Li Y., Lu L.;
RT "PLAB, a novel placental bone morphogenetic protein.";
RL Biochim. Biophys. Acta 1354:40-44(1997).
[4]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98256302; PubMed=9593718; DOI=10.1074/jbc.273.22.13760;
RA Paralkar V.M., Vail A.L., Grasser W.A., Brown T.A., Xu H., Vukicevic S., Ke H.Z., Qi H., Owen T.A., Thompson D.D.;
RT "Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family.";
RL J. Biol. Chem. 273:13760-13767(1998).
[5]
RN SEQUENCE OF 14-308 FROM N.A.
RX MEDLINE=98085971; PubMed=9426002; DOI=10.1016/S0378-1119(97)00485-X;
RA Lawton L.N., de Fatima Bonaide M., Jelenc P.C., Qiu L., Baumes S.A., Marcelino R.A., de Jesus G.M., Wellington S., Knowles J.A.,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 8.53861 Seconds
(without alignments)
1104.306 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111
Perfect score: 541
Sequence: 1 CCRLLHTVRASLDLGWADWV.....TDTGVSLOTQYDILLAKDCHC 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	309	2 JC5697	placental transfor
2	201	37.2	365	2 T43286	cet-1 protein - Ca
3	191	35.3	430	2 J01184	osteogenic protein
4	191	35.3	513	1 EMH06	bone morphogenetic
5	188	34.8	207	2 S37618	vgr protein - rat
6	188	34.8	426	2 JH0690	bone morphogenetic
7	188	34.8	510	2 A54798	Vg-1-related prote
8	187	34.6	313	2 I51284	bone morphogenetic
9	187	34.6	431	1 EMH07	bone morphogenetic
10	187	34.6	455	2 A43918	TGF-beta-related p
11	184	34.0	452	2 I49542	bone morphogenetic
12	184	34.0	454	1 EMH05	bone morphogenetic
13	181	33.5	360	2 A29619	Vgl embryonic grow
14	173	32.0	151	2 S43296	bone morphogenetic
15	173	32.0	402	2 A45056	osteogenic protein
16	172	31.8	441	2 S45284	growth/differentia
17	170	31.4	588	2 A26158	decapentaplegic pr
18	168	31.1	495	2 S43294	bone morphogenetic
19	168	31.1	501	2 JC2347	growth/differentia
20	168	31.1	501	2 A55452	cartilage-derived
21	164	30.4	354	2 S29718	gene nodal protein
22	163	30.1	461	2 S24408	SPDVR1 protein - s
23	161	29.8	125	2 S43295	bone morphogenetic
24	160	29.7	366	2 A46607	growth/differentia
25	159	29.4	372	2 C39364	GDF-1 embryonic gr
26	156	28.8	436	2 B55452	cartilage-derived
27	155	28.7	366	2 A45402	transforming growt
28	152	28.2	357	2 A39364	GDF-1 embryonic gr
29	150	27.8	350	2 JC5241	activin beta E cha

30	147.5	27.3	401	2 JH0689	bone morphogenetic
31	147.5	27.3	408	1 EMH04	bone morphogenetic
32	147.5	27.3	408	2 S58791	bone morphogenetic
33	147.5	27.3	408	2 S38343	bone morphogenetic
34	147.5	27.3	420	2 T49541	bone morphogenetic
35	147.5	27.3	427	2 A40735	TGF beta homolog d
36	146.5	27.1	400	2 A49147	bone morphogenetic
37	146.5	27.1	405	2 T50608	bone morphogenetic
38	146.5	27.1	476	2 JC4646	bone morphogenetic
39	144.5	26.7	472	1 EMH03	bone morphogenetic
40	143.5	26.5	360	2 I53032	bone morphogenetic
41	143.5	26.5	398	2 JH0688	bone morphogenetic
42	143.5	26.5	398	2 JH0687	bone morphogenetic
43	143.5	26.5	478	2 JC4838	bone morphogenetic
44	141	26.1	365	2 T03907	TGF-beta-related p
45	140.5	26.0	408	2 JH0801	bone morphogenetic

ALIGNMENTS

RESULT 1

JC5697

Placental transforming growth factor-beta homolog - human
C/Species: Homo sapiens (man)

C/Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004

C/Accession: JC5697

R:Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.

J. Biochem. 122, 622-626, 1997

A/Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in

A/Reference number: JC5697; MUID:98006316; PMID:9348093

A/Accession: JC5697

A/Molecule type: mRNA

A/Residues: 1-309 <YOK>

A/Cross-references: UNIPROT:Q9BWA0; DDBJ:AB000584

A/Experimental source: fibrosarcoma

C/Comment: This protein plays a role in reproduction.

Query Match 100.0%; Score 541; DB 2; Length 309;

Best Local Similarity 100.0%; Pred. No. 5.8e-51;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCRLLHTVRASLDLGWADWVLSPREVQVTCIGACPSQFRAANWHAQIKTSLRLKPDTV 60

Db 211 CCRLLHTVRASLDLGWADWVLSPREVQVTCIGACPSQFRAANWHAQIKTSLRLKPDTV 270

Cy 61 PAPCCVPASYNPMVLIQKTDGTGVSLOTQYDILLAKDCHC 98

Db 271 PAPCCVPASYNPMVLIQKTDGTGVSLOTQYDILLAKDCHC 308

RESULT 2

T43286

cet-1 protein - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T43286

R:Morita, K.; Chow, K.L.; Ueno, N.

Development 126, 1337-1347, 1999

A/Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis

A/Reference number: 222393; MUID:99146896; PMID:10021351

A/Accession: T43286

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-365 <MOR>

A/Cross-references: UNIPROT:O76514; EMBL:AF074395; NID:G3328181; PIDN:AAC26791.1; PID:9

C/Genetics:

A/Gene: cet-1

A/Map position: 5

C/Superfamily: inhibin

Query Match 37.2%; Score 201; DB 2; Length 365;

Best Local Similarity 36.3%; Pred. No. 4.3e-14;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:29:15 ; Search time 63 Seconds
(without alignments)
601.627 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111
Perfect score: 541
Sequence: 1 CCRLLHTVRASLEDLGWADWV.....TDTGVSLQTYDLLAKDCHC 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	112	2	AAR84709 Human emb
2	541	100.0	112	4	AAB36558 Human GDF
3	541	100.0	119	2	AAW31509 Growth di
4	541	100.0	141	2	AAW10674 TGF-beta-
5	541	100.0	154	2	AAW10665 Human TGF
6	541	100.0	203	2	AAW10664 Human TGF
7	541	100.0	283	8	ADJ87287 Human G p
8	541	100.0	295	4	AAB36557 Human GDF
9	541	100.0	308	2	AAR77097 Human TGF
10	541	100.0	308	2	AAR84710 Human emb
11	541	100.0	308	2	AAW10673 Human TGF
12	541	100.0	308	2	AAW10666 Human TGF
13	541	100.0	308	2	AAW10670 Human TGF
14	541	100.0	308	2	AAW10672 Human TGF
15	541	100.0	308	2	AAW10669 Human TGF
16	541	100.0	308	2	AAW10662 Human TGF
17	541	100.0	308	2	AAW10668 Human TGF
18	541	100.0	308	2	AAW10667 Human TGF
19	541	100.0	308	2	AAW10671 Human TGF
20	541	100.0	308	2	AAW48672 GF-2H pro
21	541	100.0	308	3	AAB26122 Human TGF
22	541	100.0	308	5	AB090174 Human NAG
23	541	100.0	308	5	AAE13538 Human mac
24	541	100.0	308	5	AAE13539 Human mac
25	541	100.0	308	6	ADA11070 Human cDN

ALIGNMENTS

RESULT 1
AAR84709

ID AAR84709 standard; protein; 112 AA.

AC AAR84709;

DT 23-MAY-1996 (first entry)

DE Human embryonal lung mature protein.

XX Eosinophil; inhibitor; active oxygen production; bronchial asthma; human;
KW embryonal lung.

OS Homo sapiens.

PN JP07258293-A.

XX 09-OCT-1995.

PF 23-MAR-1994; 94JP-00052225.

PR 23-MAR-1994; 94JP-00052225.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1995-380074/49.

DR N-PSDB; AAT05177.

XX A new protein for the treatment of bronchial asthma - inhibits the
PT production of active oxygen in eosinophil(s).

PS Claim 1; Page 2; 26pp; Japanese.

CC The present sequence is that of a 112 amino acid mature protein isolated
from normal diploid cells of human embryonal lung tissue. The protein
inhibits production of active oxygen in eosinophils and is useful for
treatment and prevention of bronchial asthma

SQ Sequence 112 AA;

Query Match 100.0%; Score 541; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.3e-51;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRLLHTVRASLEDLGWADWVLSPREVQVTWCIGACPSQFRAANHHQAQIKTSLHRLKPDV 60

Db 14 CCRLLHTVRASLEDLGWADWVLSPREVQVTWCIGACPSQFRAANHHQAQIKTSLHRLKPDV 73